

Jaap Heringa

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

9,443
citations

687363

13
h-index

610901

24
g-index

26
all docs

26
docs citations

26
times ranked

21004
citing authors

#	ARTICLE	IF	CITATIONS
1	PIPENN: protein interface prediction from sequence with an ensemble of neural nets. <i>Bioinformatics</i> , 2022, 38, 2111-2118.	4.1	10
2	A framework for exhaustive modelling of genetic interaction patterns using Petri nets. <i>Bioinformatics</i> , 2020, 36, 2142-2149.	4.1	3
3	FAIR Principles: Interpretations and Implementation Considerations. <i>Data Intelligence</i> , 2020, 2, 10-29.	1.5	149
4	Tailor-made multiple sequence alignments using the PRALINE 2 alignment toolkit. <i>Bioinformatics</i> , 2019, 35, 5315-5317.	4.1	4
5	Leveraging European infrastructures to access 1 million human genomes by 2022. <i>Nature Reviews Genetics</i> , 2019, 20, 693-701.	16.3	69
6	The potential use of big data in oncology. <i>Oral Oncology</i> , 2019, 98, 8-12.	1.5	40
7	SeRenDIP: SEquential REmasteriNg to Derive profiles for fast and accurate predictions of PPI interface positions. <i>Bioinformatics</i> , 2019, 35, 4794-4796.	4.1	21
8	Bioinformatics in the Netherlands: the value of a nationwide community. <i>Briefings in Bioinformatics</i> , 2019, 20, 375-383.	6.5	15
9	Motif-Aware PRALINE: Improving the alignment of motif regions. <i>PLoS Computational Biology</i> , 2018, 14, e1006547.	3.2	7
10	Training for translation between disciplines: a philosophy for life and data sciences curricula. <i>Bioinformatics</i> , 2018, 34, i4-i12.	4.1	5
11	Aurora kinase A (AURKA) interaction with Wnt and Ras-MAPK signalling pathways in colorectal cancer. <i>Scientific Reports</i> , 2018, 8, 7522.	3.3	38
12	Seeing the trees through the forest: sequence-based homo- and heteromeric protein-protein interaction sites prediction using random forest. <i>Bioinformatics</i> , 2017, 33, 1479-1487.	4.1	66
13	Both Intrinsic Substrate Preference and Network Context Contribute to Substrate Selection of Classical Tyrosine Phosphatases. <i>Journal of Biological Chemistry</i> , 2017, 292, 4942-4952.	3.4	8
14	Bridging the translational innovation gap through good biomarker practice. <i>Nature Reviews Drug Discovery</i> , 2017, 16, 587-588.	46.4	48
15	Systematically linking tranSMART, Galaxy and EGA for reusing human translational research data. <i>F1000Research</i> , 2017, 6, 1488.	1.6	8
16	Construction and Experimental Validation of a Petri Net Model of Wnt/ β -Catenin Signaling. <i>PLoS ONE</i> , 2016, 11, e0155743.	2.5	16
17	The FAIR Guiding Principles for scientific data management and stewardship. <i>Scientific Data</i> , 2016, 3, 160018.	5.3	8,670
18	Integration of EGA secure data access into Galaxy. <i>F1000Research</i> , 2016, 5, 2841.	1.6	7

#	ARTICLE	IF	CITATIONS
19	Sequence specificity between interacting and non-interacting homologs identifies interface residues – a homodimer and monomer use case. BMC Bioinformatics, 2015, 16, 325.	2.6	18
20	Multi-Harmony: detecting functional specificity from sequence alignment. Nucleic Acids Research, 2010, 38, W35-W40.	14.5	51
21	Multi-RELIEF: a method to recognize specificity determining residues from multiple sequence alignments using a Machine-Learning approach for feature weighting. Bioinformatics, 2008, 24, 18-25.	4.1	83
22	Sequence harmony: detecting functional specificity from alignments. Nucleic Acids Research, 2007, 35, W495-W498.	14.5	34
23	Sequence comparison by sequence harmony identifies subtype-specific functional sites. Nucleic Acids Research, 2006, 34, 6540-6548.	14.5	64